



## Searching for SNPs between Mouse Strains

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### Could you tell me the names and the number of the mouse strains for which dbSNP has data? How do I access this data?

There is no listing of SNPs across all mouse strains. You can [search between strains](#), and you can get a listing of all the mouse SNPs in dbSNP by [searching Entrez SNP](#) or downloading the mouse data from the [dbSNP FTP site](#). (01/15/08)

### After narrowing the range of my search for SNPs that are polymorphic between the C57BL6/J and 129 sv/j strains of mice by typing 3[CHR]105351425:107237468 [CHRPOS] into EntrezSNP, How do I get Entrez SNP to show me SNPs that are polymorphic between C57BL6/J and 129 sv/j?

Enter the following into Entrez SNP:

```
"Mouse[orgn] AND true[gtype] AND 3[CHR] AND 105351425:107237468 [CHRPOS]"
```

(11/06:02/14)

### I want to find SNPs in the 129 and Bl6 mouse strains that are the same as each other but differ from BALB/c using the Search Mouse SNP between strains tool. I stipulated that BALB/c was to differ from 129/Sv, 129X1/SVJ, 129X1/SV, C57BL/6, C57BL/6J, and *Mus musculus* C57BL/6J. This query returns extra SNPs that do not conform to my requirements.

The Search Mouse SNP between strains tool will return any SNPs that are different between strain BALB/c and strains 129 or C57BL. It does not work for your query where SNPs have to be common between strains 129 and C57BL and different from BALB/c.

The way to get around this problem is to perform two searches:

First, perform a search using the Search Mouse SNP between strains tool, where you ask for those SNPs that are different between reference strain BALB/c and strains 129/Sv, 129X1/SVJ, 129X1/SV, C57BL/6, C57BL/6J, and *Mus musculus* C57BL/6J. Then perform a second search using the Search Mouse SNP between strains tool, where you ask for those SNPs that are found in common between reference strain 129/Sv and strains C57BL/6, C57BL/6J, and *Mus musculus* C57BL/6J.

Save the results from each search file in the brief format, and then filter for the SNPs (rs#) that are in both files.